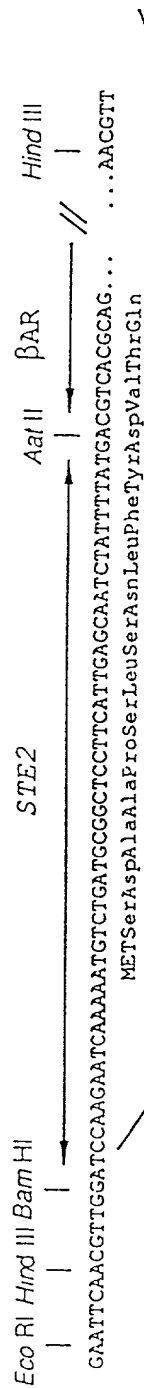


A.



B.

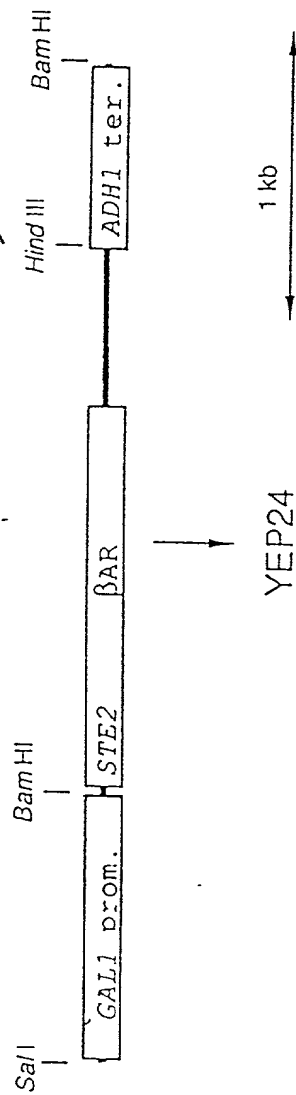


FIG. 1

Figure 1 consists of two panels, A and B, showing the binding of ^{125}I -CYP to CYP1A2 and CYP1A1, respectively. Both panels use a semi-logarithmic scale where the x-axis represents the concentration of ^{125}I -CYP in nM (log scale from 0.01 to 0.4) and the y-axis represents the amount of ^{125}I -CYP bound in pmol (linear scale from 0.0 to 6.0).

Panel (A) shows the binding to CYP1A2. The data points (filled circles) follow a saturation curve, indicating a finite number of binding sites. The binding increases rapidly at low concentrations and then levels off. A solid line represents the best fit to the data.

Panel (B) shows the binding to CYP1A1. The data points (filled squares) follow a linear relationship, indicating that the binding is non-saturable within the tested concentration range. A solid line represents the best fit to the data.

^{125}I -CYP (nM)	^{125}I -CYP Bound (pmol)	
	CYP1A2 (Panel A)	CYP1A1 (Panel B)
0.01	0.2	0.1
0.015	0.4	0.2
0.02	0.9	0.2
0.03	1.4	0.3
0.05	1.8	0.4
0.1	3.2	0.9
0.4	5.2	3.1

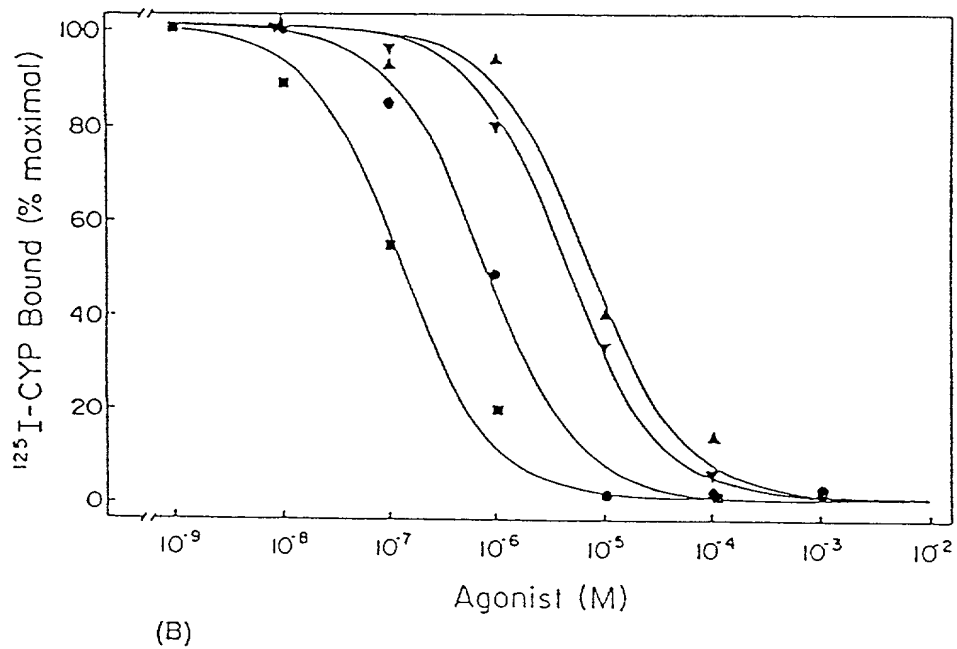


FIG. 2

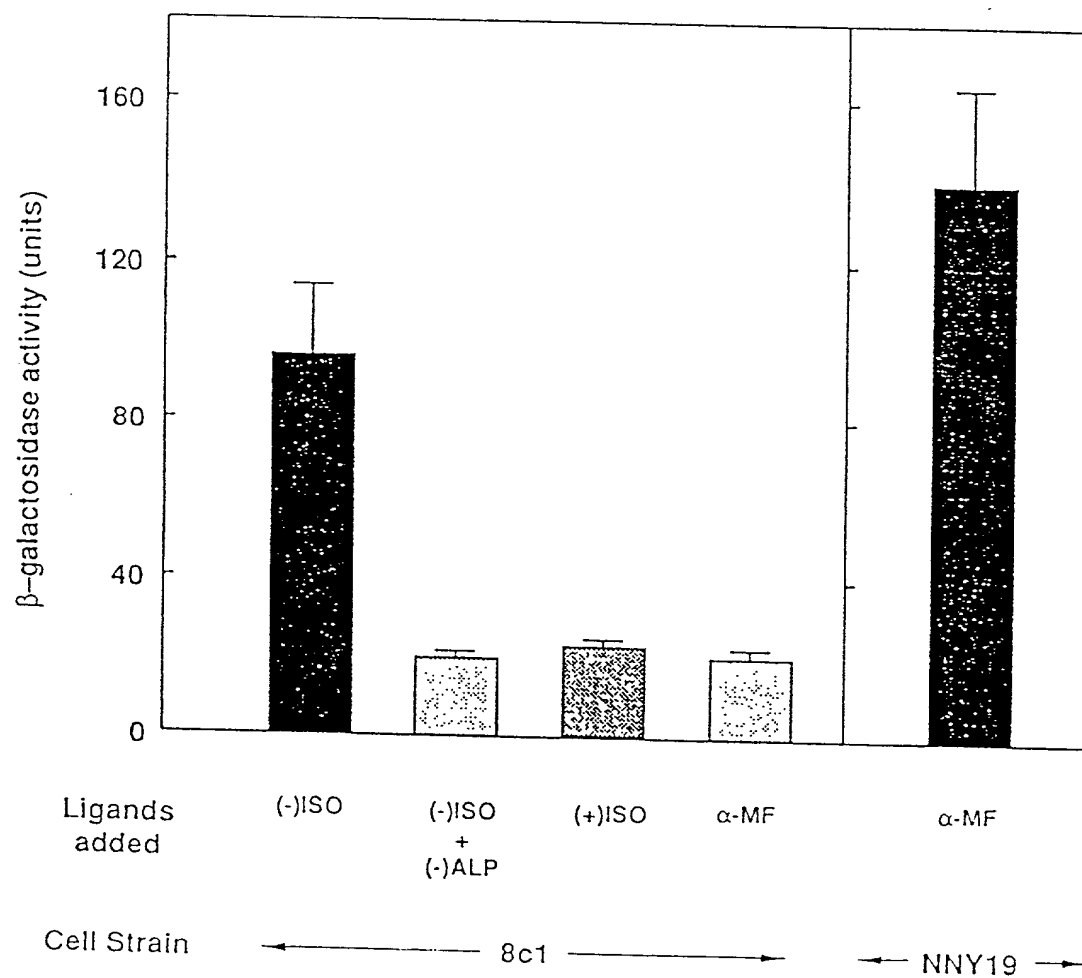


FIG. 3